

**IN THE UNITED STATES DISTRICT COURT  
FOR THE DISTRICT OF DELAWARE**

CELLECTIS S.A.,

Plaintiff,

V.

PRECISION BIOSCIENCES, INC.,

Defendant.

C.A. No. 11-173-SLR-MPT

### JOINT CLAIM CONSTRUCTION CHART

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Claim Term	Plaintiff's Proposed Construction <sup>1</sup>	Defendant's Proposed Construction
monomer of an I-CreI meganuclease variant	a polypeptide from an I-CreI meganuclease variant	one of two polypeptides, each having a single copy of the dodecapeptide (LAGLIDADG) motif, that can act together to form an I-CreI variant homodimer
monomer of an I-CreI meganuclease variant comprising at least one mutation in the amino acid sequence of SEQ ID NO: 70, wherein said at least one mutation comprises a substitution at one or more of the amino acid residues at positions 44, 68 and 70 and said monomer further comprises at least one additional mutation of an amino acid residue directly contacting a DNA target sequence wherein said amino acid residue directly contacting a DNA target sequence is selected from the group consisting of positions 26, 28, 30, 32, 33 and 38	monomer of an I-CreI meganuclease variant comprising at least one mutation in the amino acid sequence of SEQ ID NO: 70, wherein said at least one mutation comprises a substitution at one or more of the amino acid residues at positions 44, 68 and 70 with reference to the amino acid numbering of SwissProt accession number P05725 or pdb accession code 1g9y and said monomer further comprises at least one additional mutation of an amino acid residue at positions 26, 28, 30, 32, 33 or 38 with reference to the amino acid numbering of SwissProt accession number P05725 or pdb accession code 1g9y	monomer of an I-CreI meganuclease variant having the amino acid sequence of SEQ ID NO: 70 in which from 1-3 of the amino acids corresponding to positions 44, 68 and 70 of wild-type I-CreI and from 1-6 of the amino acids corresponding to positions 26, 28, 30, 32, 33 and 38 of wild-type I-CreI have been substituted with different amino acids

<sup>1</sup> It is Plaintiff's position that the Court need not construe all of the terms provided in this table as the meaning of the terms and phrases included in the chart are clear based on their well-understood ordinary meanings or the use of the terms in the claims, specification and prosecution history of the patent in suit. Plaintiff is providing constructions to the terms and phrases set forth below because these terms and phrases have been identified by Defendant. Plaintiff provided proposed constructions in the event that the Court decides that construction is necessary.

Claim Term	Plaintiff's Proposed Construction	Defendant's Proposed Construction
<p>modified DNA cleavage specificity relative to the I-CreI meganuclease of SEQ ID NO: 70 in at least one nucleotide in the +/- 3 to 5 triplets</p>	<p>having the ability to cleave a DNA target site that has at least one nucleotide mutation in the gtc triplet at positions -5 to -3 or the gac triplet at positions +3 to +5, where the DNA target site is not cleaved in the same conditions by an initial meganuclease scaffold</p>	<p>having cleavage specificity for a DNA target having the nucleotide sequence 5'-R<sub>1</sub>CAAAR<sub>2</sub>R<sub>3</sub>R<sub>4</sub>R'<sub>3</sub>R'<sub>4</sub>R'<sub>2</sub>TTTG R'<sub>1</sub>-3' where</p> <p>R<sub>1</sub> is any sequence of 0-9 of the nucleotides g, t, c and a;</p> <p>R<sub>2</sub> is ac or ct;</p> <p>R<sub>3</sub> is any sequence of 3 of the nucleotides g, t, c and a except gtc, gcc, gtg, gtt and gct;</p> <p>R<sub>4</sub> is gt or tc;</p> <p>R'<sub>4</sub> is ga or ac;</p> <p>R'<sub>3</sub> is any sequence of 3 of the nucleotides g, t, c and a;</p> <p>R'<sub>2</sub> is ag or gt; and</p> <p>R'<sub>1</sub> is any sequence of 0-9 of the nucleotides g, t, c and a</p>

<b>Claim Term</b>	<b>Plaintiff's Proposed Construction</b>	<b>Defendant's Proposed Construction</b>
A44/A68/A70 ... T44/S68/K70	The nomenclature "X"44/"Y"68/"Z"70 means a variant monomer having amino acid residues, "X," "Y" and "Z" at position 44, 68 and 70 with reference to the amino acid numbering of SwissProt accession number P05725 or pdb accession code 1g9y	The nomenclature "X"44/"Y"68/"Z"70 means a variant having amino acid residues "X," "Y" and "Z" at positions corresponding, respectively, to positions 44, 68 and 70 of a wild-type monomer from I-CreI
single-chain chimeric meganuclease comprising [a] fusion of [two monomers]	a meganuclease in the form of a single protein comprising a first monomer fused to a second monomer	a meganuclease in the form of a single polypeptide comprising a first monomer fused to a second monomer
variant of the wild-type monomer from I-CreI	a mutant monomer of I-CreI, which when in dimeric form, retains the ability to cleave DNA	<b>Indefinite under 35 U.S.C. 112, ¶2</b>
wild-type monomer from I-DmI	a naturally occurring amino acid sequence from I-DmI that has the ability to cleave DNA when in dimeric form with a monomer of I-CreI	a meganuclease monomer having the amino acid sequence of PDB accession number 1b24
variant of the wild-type monomer from I-DmI	a mutant monomer of I-DmI that has the ability to cleave DNA when in dimeric form with a monomer of I-CreI	<b>Indefinite under 35 U.S.C. 112, ¶2</b>

### Glossary of Agreed Upon Terms

Glossary Term	Definition
recombinant	genetically engineered
monomer	a molecular building block—e.g., a polypeptide—that can be associated with another to form a larger molecule
when in a dimeric form	when two monomers are associated
homodimer	a complex composed of two identical monomers
I-CreI meganuclease variant homodimer	a variant of an I-CreI meganuclease composed of two identical monomers
heterodimer	a complex composed of two different monomers
I-CreI meganuclease variant heterodimer	a variant of an I-CreI meganuclease composed of two different monomers
wild-type monomer from I-CreI	a monomer having the amino acid sequence of SwissProt accession number P05725 or pdb accession code 1g9y